

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/001,039BDATE: 05/11/2000  
TIME: 18:16:21

INPUT SET: S35468.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANTS: Jolly, Douglas J.  
6 Chang, Stephen M.W.  
7 Respass, James G.  
8 DePollo, Nicholas J.  
9 Hsu, David Chi-Tang  
10 Ibanez, Carlos E.  
11 Greengard, Judith  
12 Lee, Will  
13  
14 (ii) TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF  
15 RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT  
16 OF HEMOPHILIA AND OTHER DISORDERS  
17  
18 (iii) NUMBER OF SEQUENCES: 84  
19  
20 (iv) CORRESPONDENCE ADDRESS:  
21 (A) ADDRESSEE: Seed Intellectual Property Law Group  
22 (B) STREET: 701 Fifth Avenue, Suite 6300  
23 (C) CITY: Seattle  
24 (D) STATE: Washington  
25 (E) COUNTRY: U.S.A.  
26 (F) ZIP: 98104  
27  
28 (v) COMPUTER READABLE FORM:  
29 (A) MEDIUM TYPE: Floppy disk  
30 (B) COMPUTER: IBM PC compatible  
31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
33  
34 (vi) CURRENT APPLICATION DATA:  
35 (A) APPLICATION NUMBER: US 09/001,039  
36 (B) FILING DATE: 13-JAN-1998  
37 (C) CLASSIFICATION:  
38  
39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: McMasters, David D.  
41 (B) REGISTRATION NUMBER: 33,963  
42 (C) REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4  
43  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: (206) 622-4900  
46 (B) TELEFAX: (206) 682-6031

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47  
48  
49  
50 (2) INFORMATION FOR SEQ ID NO:1:  
51 (i) SEQUENCE CHARACTERISTICS:  
52 (A) LENGTH: 24 base pairs  
53 (B) TYPE: nucleic acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear  
56 (ii) MOLECULE TYPE: DNA (genomic)  
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
58 GAGAGATGGG GGAGGCTAAC TGAG 24  
59  
60 (2) INFORMATION FOR SEQ ID NO:2:  
61 (i) SEQUENCE CHARACTERISTICS:  
62 (A) LENGTH: 28 base pairs  
63 (B) TYPE: nucleic acid  
64 (C) STRANDEDNESS: single  
65 (D) TOPOLOGY: linear  
66 (ii) MOLECULE TYPE: DNA (genomic)  
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
68 GATCCTCAGT TAGCCTCCCC CATCTCTC 28  
69  
70 (2) INFORMATION FOR SEQ ID NO:3:  
71 (i) SEQUENCE CHARACTERISTICS:  
72 (A) LENGTH: 35 base pairs  
73 (B) TYPE: nucleic acid  
74 (C) STRANDEDNESS: single  
75 (D) TOPOLOGY: linear  
76 (ii) MOLECULE TYPE: DNA (genomic)  
77 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
78 TATATCTCCA GATGAGGTAC ATGATTTTAG GCTTG 35  
79  
80 (2) INFORMATION FOR SEQ ID NO:4:  
81 (i) SEQUENCE CHARACTERISTICS:  
82 (A) LENGTH: 40 base pairs  
83 (B) TYPE: nucleic acid  
84 (C) STRANDEDNESS: single  
85 (D) TOPOLOGY: linear  
86 (ii) MOLECULE TYPE: DNA (genomic)  
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
88 TATATATCGA TTCAAGGCAT TTTCTTTTCA TCAATAAAAC 40  
89  
90 (2) INFORMATION FOR SEQ ID NO:5:  
91 (i) SEQUENCE CHARACTERISTICS:  
92 (A) LENGTH: 37 base pairs  
93 (B) TYPE: nucleic acid  
94 (C) STRANDEDNESS: single  
95 (D) TOPOLOGY: linear  
96 (ii) MOLECULE TYPE: DNA (genomic)  
97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
98 TCGAGGATCC GCGCGGCGG CCGCATCGAT GTCGACG 37  
99

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100 (2) INFORMATION FOR SEQ ID NO:6:  
101 (i) SEQUENCE CHARACTERISTICS:  
102 (A) LENGTH: 35 base pairs  
103 (B) TYPE: nucleic acid  
104 (C) STRANDEDNESS: single  
105 (D) TOPOLOGY: linear  
106 (ii) MOLECULE TYPE: DNA (genomic)  
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
108 CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC 35  
109  
110  
111 (2) INFORMATION FOR SEQ ID NO:7:  
112 (i) SEQUENCE CHARACTERISTICS:  
113 (A) LENGTH: 77 base pairs  
114 (B) TYPE: nucleic acid  
115 (C) STRANDEDNESS: single  
116 (D) TOPOLOGY: linear  
117 (ii) MOLECULE TYPE: DNA (genomic)  
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
119 AGTGAATTCG AGCTCGGTAC CCGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT 60  
120 GGCGTACTCA TGGTCAT 77  
121  
122 (2) INFORMATION FOR SEQ ID NO:8:  
123 (i) SEQUENCE CHARACTERISTICS:  
124 (A) LENGTH: 8 amino acids  
125 (B) TYPE: amino acid  
126 (C) STRANDEDNESS: single  
127 (D) TOPOLOGY: linear  
128 (ii) MOLECULE TYPE: protein  
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
130 Ala Arg Glu Met Gly Glu Ala Asn  
131 1 5  
132  
133 (2) INFORMATION FOR SEQ ID NO:9:  
134 (i) SEQUENCE CHARACTERISTICS:  
135 (A) LENGTH: 27 base pairs  
136 (B) TYPE: nucleic acid  
137 (C) STRANDEDNESS: single  
138 (D) TOPOLOGY: linear  
139 (ii) MOLECULE TYPE: DNA (genomic)  
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
141 CCCGAGAGAT GGGGGAGGCT AACTGAG 27  
142  
143 (2) INFORMATION FOR SEQ ID NO:10:  
144 (i) SEQUENCE CHARACTERISTICS:  
145 (A) LENGTH: 31 base pairs  
146 (B) TYPE: nucleic acid  
147 (C) STRANDEDNESS: single  
148 (D) TOPOLOGY: linear  
149 (ii) MOLECULE TYPE: DNA (genomic)  
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
151 GGGCTCTCTA CCCCTCCGA TTGACACCTA G 31  
152

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153 (2) INFORMATION FOR SEQ ID NO:11:  
154 (i) SEQUENCE CHARACTERISTICS:  
155 (A) LENGTH: 5 amino acids  
156 (B) TYPE: amino acid  
157 (C) STRANDEDNESS: single  
158 (D) TOPOLOGY: linear  
159 (ii) MOLECULE TYPE: protein  
160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
161 Thr Ile Met Thr Met  
162 1 5  
163  
164

165 (2) INFORMATION FOR SEQ ID NO:12:  
166 (i) SEQUENCE CHARACTERISTICS:  
167 (A) LENGTH: 24 base pairs  
168 (B) TYPE: nucleic acid  
169 (C) STRANDEDNESS: single  
170 (D) TOPOLOGY: linear  
171 (ii) MOLECULE TYPE: DNA (genomic)  
172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
173 CCCTGTGCCT TATTTGAACT AACC 24  
174

175 (2) INFORMATION FOR SEQ ID NO:13:  
176 (i) SEQUENCE CHARACTERISTICS:  
177 (A) LENGTH: 24 base pairs  
178 (B) TYPE: nucleic acid  
179 (C) STRANDEDNESS: single  
180 (D) TOPOLOGY: linear  
181 (ii) MOLECULE TYPE: DNA (genomic)  
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
183 CCCACCACAA CCACATATCC CTCC 24  
184

185 (2) INFORMATION FOR SEQ ID NO:14:  
186 (i) SEQUENCE CHARACTERISTICS:  
187 (A) LENGTH: 19 base pairs  
188 (B) TYPE: nucleic acid  
189 (C) STRANDEDNESS: single  
190 (D) TOPOLOGY: linear  
191 (ii) MOLECULE TYPE: DNA (genomic)  
192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
193 CCAGTCCTCC GATTGACTG 19  
194

195 (2) INFORMATION FOR SEQ ID NO:15:  
196 (i) SEQUENCE CHARACTERISTICS:  
197 (A) LENGTH: 8332 base pairs  
198 (B) TYPE: nucleic acid  
199 (C) STRANDEDNESS: single  
200 (D) TOPOLOGY: linear  
201 (ii) MOLECULE TYPE: DNA (genomic)  
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
203  
204 GCGCCAGTCC TCCGATTGAC TGAGTCGCCC GGGTACCCGT GATCCAATA AACCTCTTG 60  
205

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206	CAGTTGCATC	CGACTTGTGG	TCTCGCTGTT	CCTTGGGAGG	GTCTCCTCTG	AGTGATTGAC	120
207							
208	TACCCGTCAG	CGGGGGTCTT	TCATTTGGGG	GCTCGTCCGG	GATCGGGAGA	CCCCTGCCCA	180
209							
210	GGGACCACCG	ACCCACCACC	GGGAGGTAAG	CTGGCCAGCA	ACTTATCTGT	GTCTGTCCGA	240
211							
212	TTGTCTAGTG	TCTATGACTG	ATTTTATGCG	CCTGCGTCGG	TACTAGTTAG	CTAACTAGCT	300
213							
214	CTGTATCTGG	CGGACCCGTG	GTGGAAGTGA	CGAGTTCGGA	ACACCCGGCC	GCAACCCTGG	360
215							
216	GAGACGTCCC	AGGGACTTCG	GGGGCCGTTT	TTGTGGCCCC	ACCTGAGTCC	AAAAATCCCG	420
217							
218	ATCGTTTTGG	ACTCTTTGGT	GCACCCCCCT	TAGAGGAGGG	ATATGTGGTT	CTGGTAGGAG	480
219							
220	ACGAGAACCT	AAAACAGTTC	CCGCCTCCGT	CTGAATTTTT	GCTTTCGGTT	TGGGACCGAA	540
221							
222	GCCGCGCCGC	GCGTCTTGTC	TGCTGCAGCA	TCGTTCTGTG	TTGTCTCTGT	CTGACTGTGT	600
223							
224	TTCTGTATTT	GTCTGAGAAT	ATGGGCCAGA	CTGTTACCAC	TCCCTTAAGT	TTGACCTTAG	660
225							
226	GTCAGTGAA	AGATGTCGAG	CGGATCGCTC	ACAACCAGTC	GGTAGATGTC	AAGAAGAGAC	720
227							
228	GTTGGGTTAC	CTTCTGCTCT	GCAGAATGGC	CAACCTTTAA	CGTCGGATGG	CCGCGAGACG	780
229							
230	GCACCTTTAA	CCGAGACCTC	ATCACCCAGG	TTAAGATCAA	GGTCTTTTCA	CCTGGCCCCG	840
231							
232	ATGGACACCC	AGACCAGGTC	CCCTACATCG	TGACCTGGGA	AGCCTTGGCT	TTTGACCCCC	900
233							
234	CTCCCTGGGT	CAAGCCCTTT	GTACACCCTA	AGCCTCCGCC	TCCTCTTCCT	CCATCCGCCC	960
235							
236	CGTCTCTCCC	CCTTGAACCT	CCTCGTTCGA	CCCCGCCTCG	ATCCTCCCTT	TATCCAGCCC	1020
237							
238	TCACTCCTTC	TCTAGGCGCC	AAACCTAAAC	CTCAAGTTCT	TTCTGACAGT	GGGGGGCCGC	1080
239							
240	TCATCGACCT	ACTTACAGAA	GACCCCCCGC	CTTATAGGGA	CCCAAGACCA	CCCCCTTCCG	1140
241							
242	ACAGGGACGG	AAATGGTGGA	GAAGCGACCC	CTGCGGGAGA	GGCACCGGAC	CCCTCCCCAA	1200
243							
244	TGGCATCTCG	CCTACGTGGG	AGACGGGAGC	CCCCTGTGGC	CGACTCCACT	ACCTCGCAGG	1260
245							
246	CATTCCCCCT	CCGCGCAGGA	GGAAACGGAC	AGCTTCAATA	CTGGCCGTTC	TCCTCTTCTG	1320
247							
248	ACCTTTACAA	CTGGAAAAAT	AATAACCCTT	CTTTTTCTGA	AGATCCAGGT	AAACTGACAG	1380
249							
250	CTCTGATCGA	GTCTGTTCTC	ATCACCCATC	AGCCCACCTG	GGACGACTGT	CAGCAGCTGT	1440
251							
252	TGGGGACTCT	GCTGACCGGA	GAAGAAAAAC	AACGGGTGCT	CTTAGAGGCT	AGAAAGGCGG	1500
253							
254	TGCGGGGCGA	TGATGGGCGC	CCCACTCAAC	TGCCCAATGA	AGTCGATGCC	GCTTTTCCCC	1560
255							
256	TCGAGCGCCC	AGACTGGGAT	TACACCACCC	AGGCAGGTAG	GAACCACCTA	GTCCACTATC	1620
257							
258	GCCAGTTGCT	CCTAGCGGGT	CTCCAAAACG	CGGGCAGAAG	CCCCACCAAT	TTGGCCAAGG	1680

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**SEQUENCE VERIFICATION REPORT**  
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